

10 30 50
-88 GTTGTCTCTGGGCAGCCAAAGTTGGCATAATTGGAAGCTTTTCCGGGCTCTGGAGGAGGGT-29

70 90 110
-28 CCTGTCTTCTTCTACAGCCGTTCCGGGCATGGCCTGGCTGGGGCGTCCGCTCCACGTCT 31
-8 M A W L G A S L H V W 11

130 150 170
32 GGGGTTGGCTAATGCTCGGCAGCTGCCCTCCTGGCCAGAGCCCAGCTGGATTCTGATGGCA 91
12 G W L M L G S C L L A R A Q L D S D G T 31

190 210 230
92 CCATCACTATAGAGGAGCAGATTGTCTTGTGCTGAAAGCGAAAGTACAATGTGAAGTCA 151
32 I T I E E Q I V L V L K A K V Q C E L N 51

250 270 290
152 ACATCACAGCTCAACTCCAGGAGGAGAGGTAATTGTTTCCCTGAATGGGATGGAGTCA 211
52 I T A Q L Q E G E G N C F P E W D G L I 71

310 330 350
212 TTTGTGGCCAGAGGAACAGTGGGAAAATATCGGCTGTTCATGCCCTCCTTATATT 271
72 C W P R G T V G K I S A V P C P Y I Y 91

370 390 410
272 ATGACTTCAACCATAAAGGAGTTGCTTCCGACACTGTAAACCCCAATGGAACATGGGATT 331
92 D F N H K G V A F R H C N P N G T W D F 111

MATCH WITH FIG. 1B

FIG. 1A

MATCH WITH FIG. 1A

332 430 TTATGCACAGCTTAAATAAACAATGGGCCAAATTATTTCAGACTGCCTTCGCTTTCTGCAGC 470 391
112 M H S L N K T W A N Y S D C L R F L Q P 131

392 490 CAGATATCAGCATAGGAAAGCAAGAATTCTGTGAACGCCCTCTATGTAATGTATACCGTTG 530 451
132 D I S I G K Q E F C E R L Y V M Y T V G 151

452 550 GCTACTCCATCICITTTGGTTCCTTGGCTGGGCTATTCATCATCAATGGTTACTTCAGAC 590 511
152 Y S I S F G S L A V A I L I I G Y F R R 171

512 610 GATTGCATTGCACTAGGAACATAATCCACATGCACCTTATTTGTGCTTTCATGCTGAGAG 650 571
172 L H C T R N Y I H M H L F V S F M L R A 191

572 670 CTACAAGCATCTTTGTCAAAGACAGAGTAGTCCATGCTCACATAGGAGTAAAGGAGCTGG 710 631
192 T S I F V K D R V V H A H I G V K E L E 211

632 730 AGTCCCTAATAATGCAGGATGACCCACAAAATTCATTGAGGCAACTTCTGTGGACAAAT 770 691
212 S L I M Q D D P Q N S I E A T S V D K S 231

790 810 830

MATCH WITH FIG. 1C

FIG. 1B

MATCH WITH FIG. 1B

692	CACAATATATCGGGTGCAAGATTGCTGTTGATGTTTATTACTTCCCTGGCTACAAATT	751
232	Q Y I G C K I A V V M F I Y F L A T N Y	251
752	ATTATTGGATCCTGGTGAAGTCTCTACCTGCATAATCTCATCTTTGTGGCTTCTTTT	811
252	Y W I L V E G L Y L H N L I F V A F F S	271
812	CGGACACCAAAATACCTGTGGGGCTTTCATCTTGATAGGCTGGGGGTTTCCAGCAGCATTTG	871
272	D T K Y L W G F I L I G W G F P A A F V	291
872	TTGCAGCATGGGCTGTGGCAGCAGCAACTCTGGCTGATGCGAGGTGCTGGGAACCTTAGTG	931
292	A A W A V A R A T L A D A R C W E L S A	311
932	CTGGAGACATCAAGTGGATTATCAAGCACCAGATCTTAGCAGCTATTGGGCTGAATTTA	991
312	G D I K W I Y Q A P I L A A I G L N F I	331
992	TTCTGTTTCTGAATACGGTTAGAGTTCTAGCTACCAAAATCTGGGAGACCAATGCAGTTG	1051
332	L F L N T V R V L A T K I W E T N A V G	351
1052	GGCATGACACAAGGAAGCAATACAGGAAACTGGCCAAATCGACACTGGTCTGTCCTAG	1111
352	H D T R K Q Y R K L A K S T L V L V L V	371

MATCH WITH FIG. 1D

FIG. 1C

MATCH WITH FIG. 1C

1210 1230 1250
1112 TCTTTGGAGTGCATTACATCGTTTCGTGTGCGCTGCTCACTCCCTTCACTGGGCTCGGGT 1171
372 F G V H Y I V F V C L P H S F T G L G W 391

1270 1290 1310
1172 GGGAGATCCGCATGCACTGTGAGCTCTTCTTCACTCCCTTTCAGGGTTTCTTTGTGCTA 1231
392 E I R M H C E L F F N S F Q G F F V S I 411

1330 1350 1370
1232 TCATCTACTGCTACTGCAATGGAGAGGTTTCAGGCAGAGGTGAAGAAGATGTGGAGTCGGT 1291
412 I Y C Y C N G E V Q A E V K K M W S R W 431

1390 1410 1430
1292 GGAATCTCTCCGTGGACTGGAAAAGGACACCCGCTATGTGGCAGCCGAGATGCGGCTCAG 1351
432 N L S V D W K R T P P C G S R R C G S V 451

1450 1470 1490
1352 TGCTCACCACCGTGCAGGCACAGCACCAGCAGCCAGTCACAGGTGGCGGCAGCACACGCAT 1411
452 L T T V T H S T S S Q S Q V A A A H A W 471

1510 1530 1550
1412 GGTGCTTATCTCTGGCAAAGCTGCCAAGATCGCCAGCAGACAGCCTGACAGCCACATCAC 1471
472 C L S L A K L P R S P A D S L T A T S L 491

MATCH WITH FIG. 1E

FIG. 1D

MATCH WITH FIG. 1D

1570	1590	1610	
1472 TTTACCTGGCTATGTCTGGAGTAACTCAGAGCAGGACTGCCTCACACACTCTCTCCACGA			1531
492 Y L A M S G V T Q S R T A S H T L S T R			511
1630	1650	1670	
1532 GGAGCAACAAGGAAGATAGTGGAGGCAGAGAGATGATATTCTAATGGAGAAGCCTTCCA			1591
512 S N K E D S G R Q R D D I L M E K P S R			531
1690	1710	1730	
1592 GGCCTATGGAATCTAACCAGACACTGAAGGATGACAAGGAGAACTGAGGATGTTCTCT			1651
532 P M E S N P D T E G			541
1750	1770	1790	
1652 GAATGGACATGTGTGGCTGACTTTTCATGGGCTGGTCCAATGGCTGTTGTGTGAGAGGC			1711
1810	1830	1850	
1712 TTGGCTGATACTCCTATGCTTGAGCACAAAGGCTGAAAATTCAGTTAAGGTGTTACTTAA			1771
1870	1890	1910	
1772 TAATAGTTTTTAGGCTCCATGAATTGGCTCCTGTAAATACTAACGACATGAAAATGCAAG			1831
1930	1950	1970	
1832 TGTCAATGGAGTAGTTTATTACCTTCTATTGGCATCAAGTTTTCCCTCTAAATTAATGTAT			1891
1990			
1892 GGTATTTGCTCTGTGATTGTTCA			1914

FIG.1E

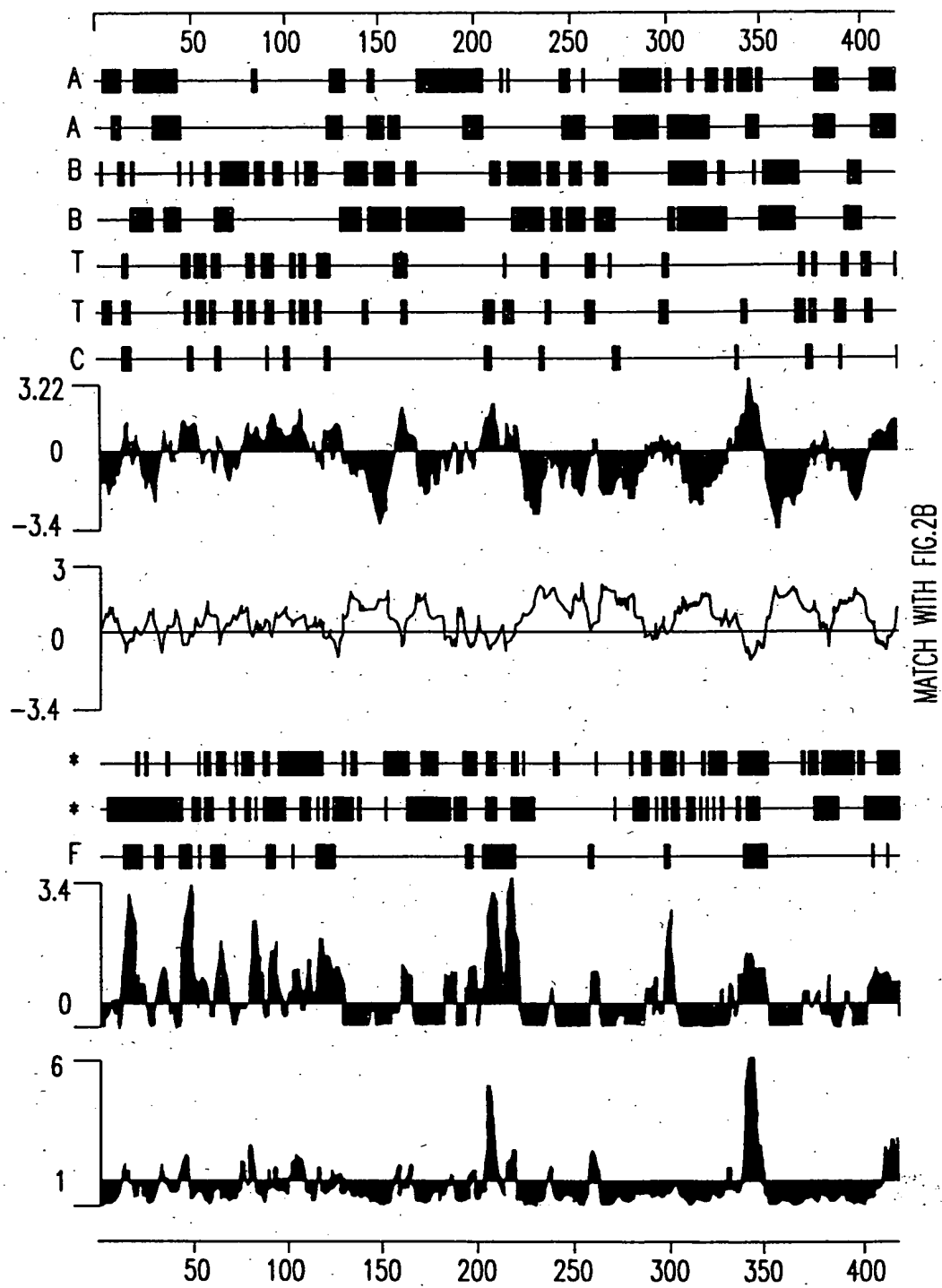


FIG. 2A

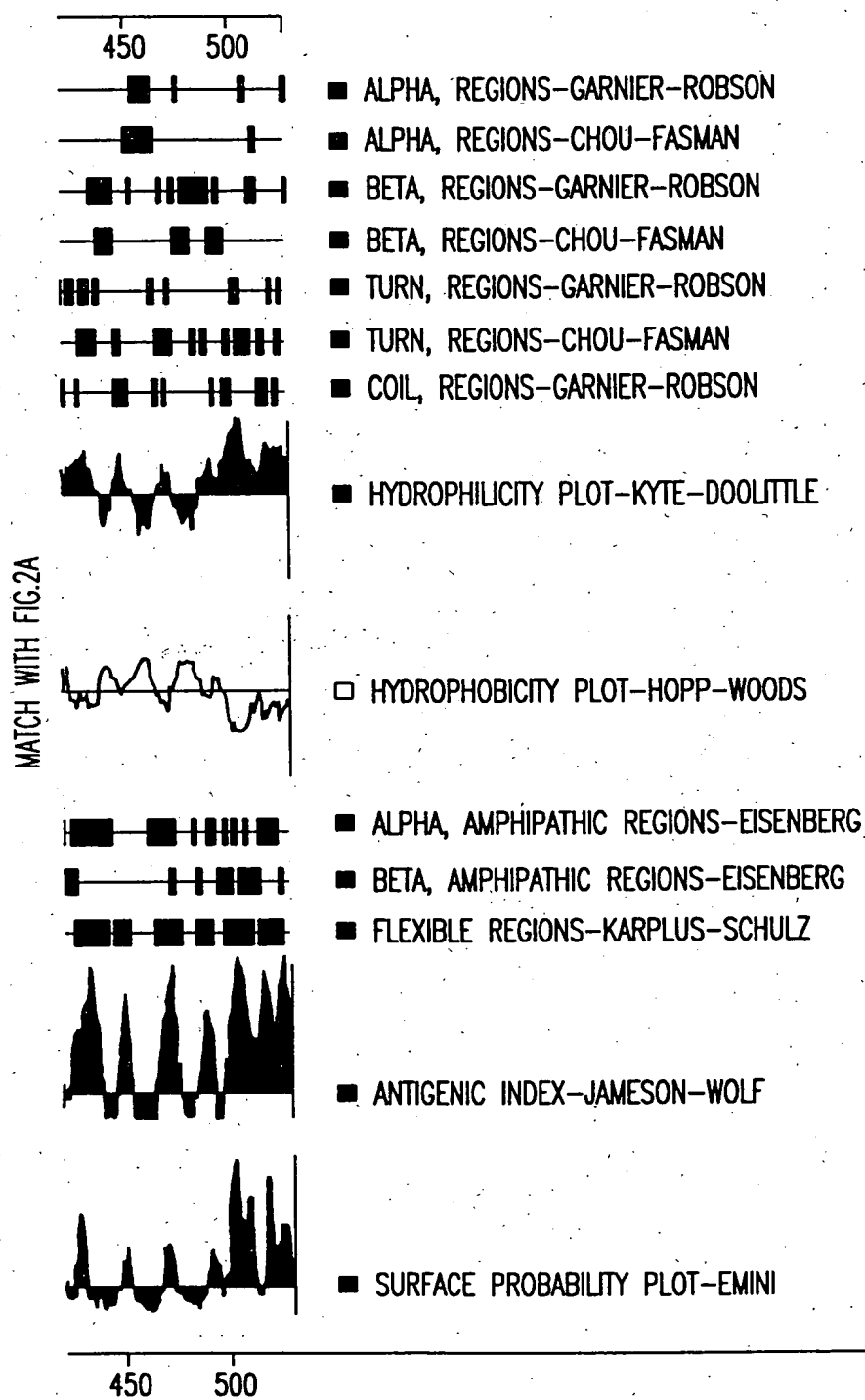


FIG. 2B

Sequences producing High-scoring Segment Pairs:		Reading High Probability		N
		Frame Score	P(N)	
gp M74445 OPOPTHYR_1	parathyroid hormone receptor [Di...	+3	597	8.2e-204
pir S A39286	parathyroid hormone / parathyroid...	+3	597	2.9e-203
gp L04308 HUMPTHYR_1	parathyroid hormone receptor [Ho...	+3	580	6.7e-190
pir S S29610	parathyroid hormone receptor - h...	+3	580	6.1e-189
gp M77184 RATPATHYR_1	parathyroid hormone receptor [Ra...	+3	576	7.7e-188
gp X78936 MPHPRR_1	parathyroid hormone/parathyroid ...	+3	576	7.7e-188
pir S A42698	parathyroid hormone and parathyr...	+3	576	7.7e-188
gp L34611 MUSPTHYR06_1	parathyroid hormone/parathyroid ...	+3	576	4.1e-174
gp U11087 HSV1RG9_1	vasoactive intestinal peptide 1 ...	+3	319	1.2e-98
gp M86835 RATVASREC_1	vasoactive intestinal polypeptid...	+3	254	3.1e-91

WARNING: Descriptions of 49 database sequences were not reported due to the limiting value of parameter $V = 10$.

>gp|M74445|OPOPTHYR_1 parathyroid hormone receptor [Didelphis virginiana]
Length = 585

Plus Strand HSPs:

Score = 597 (274.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 108/172 (62%), Positives = 136/172 (79%), Frame = +3

Match with FIG. 3B

FIG. 3A

Match with FIG. 3 A

Query: 729 IMQDDPQNSIEATSDKQYIGCKIAVWFIYFLATNYYWILVEGLYLNLFVAFSDT 908
 I +++ + E DK+ ++GC++AV +F+YFL TNYWILVEGLYLH+LIF+AFFS+
 Sbjct: 253 ITEEELRAFTPEPPADKAGFVGCRAVTVFLYFLTNYWILVEGLYHSLIFMAFFSEK 312

Query: 909 KYLWGFILIGWFPAAFWAAVARATLADARCWELSGDIKWIYQAPILAAIGLNFILF 1088
 KYLWGF L GWG PA FVA W RATLA+ CW+LS+G+ KWI Q PILAAI +NFILF
 Sbjct: 313 KYLWGFILFGWGLPAVEFVAVVTVTRATLANTECWDLSSGNKKWIIQVPILAAIVVNFILF 372

Query: 1089 LNTVRVLATKIWETNAVGHDRKQYRKLAKSTLVLVLFVGVHYIVFVCLPHS 1244
 +N +RVLATK+ ETNA DTR+QYRKL KSTLVL+ +FGVHYIVF+ P++
 Sbjct: 373 INIIRVLATKLRETNAGRCSTRQYRKLKSTLVLMPFLFGVHYIVFMATPYT 424

Score = 284 (130.6 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 42/70 (60%), Positives = 55/70 (78%), Frame = +3

Query: 267 EGNCFPEWDGLICWPRGTGKISAVPCPPYIYDFNHHKGVAFRHCNPNGTWDFMHSLNKTW 446
 +G C PEWD ++CWP G GK+ AVPCP YIYDFNHHKG A+R C+ NG+W+ + N+TW
 Sbjct: 102 DGFCLPEWDNIVCWPAGVPGKVAVVPCPDYIYDFNHHKGRAYRRCDSEWELVPGNNRTW 161

Query: 447 ANYSDCLRFL 476
 ANYS+C++FL
 Sbjct: 162 ANYSECVKFL 171

Score = 279 (128.3 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
 Identities = 51/81 (62%), Positives = 67/81 (82%), Frame = +3

Query: 498 KQEFCERLVVMYTVGYSISFGSLAVAILIIGYFRRLHCTRNYIHMHLFVSFMLRATSIFV 677
 ++E +RL ++YTVGYSIS GSL VA+LI+GYFRRLHCTRNYIHMHLFVSFMLRA SIF+

Match with FIG. 3 C

FIG. 3B

MATCH WITH FIG. 3B

Sbjct: 177 EREVFDRGLMIYTVGYSSISLGLTVAVLILGYFRRLLHCTRNYIHMHLFVSFMLRAVSIFI 236

Query: 678 KDRVVHAHIGVKELESIMQD 740

KD V+++ + E+E + ++

Sbjct: 237 KDAVLYSGVSTDEIERITEEE 257

Score = 232 (106.7 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 38/59 (64%), Positives = 50/59 (84%), Frame = +3

Query: 1248 TGLGWEIRMHCELFNFSGFFVSIICYCNGEVQAEVKMWSRWNLSDWKRTPPCGS 1424

+G+ W+++MH E+ FNSFQGFV+IIYC+CNGEVQAE+KK WSRW L++D+KR GS

Sbjct: 427 SGILWQVMHYEMLFNSFQGFVAIIYCFNCNGEVQAEIKKSWSRWTLALDFKRKARSGS 485

Score = 72 (33.1 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 16/37 (43%), Positives = 23/37 (62%), Frame = +3

Query: 159 AQLSDGTITIEEQIVLVLKAKVQCELNITAQLQEGE 269

A +D+D IT EEQI+L+ A+ QCE + L+ E

Sbjct: 24 ALVDADDVITKEEQIILLRNAQAQCEQRLKEVLRVPE 60

Score = 39 (17.9 bits), Expect = 8.2e-204, Sum P(6) = 8.2e-204
Identities = 9/23 (39%), Positives = 12/23 (52%), Frame = +2

Query: 1508 ISGKAAKIASRQPDSHITLPGYV 1576

+S + A A + H LPGYV

Sbjct: 512 LSPRLAPGAGASANGHQLPGYV 534

FIG. 3C